

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 6, 2004, 19:35:16 ; Search time 14.625 Seconds
(without alignments)
39.474 Million cell updates/sec

Title: US-10-618-644-3

Perfect score: 38

Sequence: 1 NWGPLV 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	268	2 P00199	glycinin A5A4B3 pr
2	38	100.0	484	2 S11003	glycinin G3 precu
3	38	100.0	562	1 FWSYGS	glycinin chain A5A
4	38	100.0	562	2 S20946	glycinin G4 precu
5	38	100.0	563	2 S54802	glycinin A5A4B3 ch
6	35	92.1	223	2 T41169	colicin A - Escher
7	35	92.1	387	2 S00867	colicin N - Escher
8	35	92.1	511	1 IKECBB	colicin B - Escher
9	35	92.1	592	1 IKEBCA	colicin A - Citrob
10	34	89.5	250	2 E84708	probable signal pe
11	34	89.5	265	2 F84071	hypothetical prote
12	34	89.5	367	2 E86203	probable signal pe
13	34	89.5	471	2 E50154	125K surface anti
14	34	89.5	539	2 T50435	conserved hypotet
15	34	89.5	586	1 D70413	NADH2 dehydrogenas
16	34	89.5	593	1 F70349	NADH2 dehydrogenas
17	34	89.5	639	2 A32935	protein p1 - Entam
18	34	89.5	640	2 B32935	hypothetical prote
19	34	89.5	1114	2 JH0284	125K surface anti
20	33	86.8	250	2 D72333	thiamin biosynthes
21	33	86.8	394	2 A55045	probable 3-hydroxy
22	33	86.8	491	1 S19458	hypothetical prote
23	33	86.8	615	2 D56499	probable UDP-gluc
24	32	84.2	82	1 CCPSSD	cytochrome c551 -
25	32	84.2	82	1 CCPSSP	cytochrome c551 [v
26	32	84.2	174	2 A31989	sarcoplasmic calci
27	32	84.2	174	2 S07228	calcium-binding pr
28	32	84.2	275	2 E70693	probable ugpE prot
29	32	84.2	279	2 AD2663	transcription regu

transcription regu
methionyl-tRNA for
NCA3 protein precu
spermidine/putresc
Paul protein - fis
hypothetical prote
glutamate-1-semial
glutamate-1-semial
glutamate-1-semial
glutamate-1-semial
glutamate-1-semial
glutamate-1-semial
glutamate-1-semial
tumor necrosis fac
probable membrane
proline permease (

ALIGNMENTS

RESULT 1

P00199

glycinin A5A4B3 precursor - soybean (fragment)

C;Species: Glycine max (soybean)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C;Accession: P00199

R;Scallion, B.; Thanh, V.H.; Floener, L.A.; Nielsen, N.C.

Theor. Appl. Genet. 70, 510-519, 1991

A;Title: Identification and characterization of DNA clones encoding group-II glycinin s

A;Reference number: P00199

A;Accession: P00199

A;Molecule type: DNA

A;Residues: 1-268 <SCA>

A;Cross-references: UNIPROT:Q43452; UNIPROT:Q9SB11

A;Experimental source: embryo, strain CX635-1-1-1

C;Superfamily: glycinin

C;Keywords: seed; storage protein

Query Match: 100.0%; Score 38; DB 2; Length 268;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPLV 6

Db 249 NWGPLV 254

|||||

RESULT 2

S11003

glycinin G3 precursor - soybean

C;Species: Glycine max (soybean)

C;Date: 21-Nov-1993 #sequence_revision 19-Jan-1996 #text_change 03-May-1996

C;Accession: S11003

R;Nielsen, N.C.; Dickinson, C.D.; Cho, T.J.; Thanh, V.H.; Scallion, B.J.; Fischer, R.L.

Plant Cell 1, 313-328, 1989

A;Title: Characterization of the glycinin gene family in soybean.

A;Reference number: S10851; MUID:92393391; PMID:2485233

A;Accession: S11003

A;Molecule type: DNA

A;Residues: 1-484 <NIE>

A;Experimental source: variety Dare

C;Genetics:

A;Gene: Gys3

C;Superfamily: glycinin

C;Keywords: storage protein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-484/Product: glycinin G3 #status predicted <MAT>

Query Match 100.0%; Score 38; DB 2; Length 484;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
Db 465 NWGPLV 470

RESULT 3
FWSYG5
glycinin chain A5A4B3 precursor - soybean
N/Alternate names: 11S globulin
C:Species: Glycine max (soybean)
C>Date: 28-Feb-1986 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C:Accession: A91145; A91333; A03348; A25207; A27253
R/Momma, T.; Negro, T.; Hirano, H.; Matsumoto, A.; Uda, K.; Fukazawa, C.
Eur. J. Biochem. 149, 491-496, 1985
A:Title: Glycinin A5A4B3 mRNA: cDNA cloning and nucleotide sequencing of a splitting st
A:Reference number: A91145; MUID:85230642; PMID:2988947
A:Accession: A91145
A:Molecule type: mRNA
A:Residues: 1-562 <MOM>
A:Cross-references: UNIPROT:P02858; GB:X02626; NID:g18628; PIDN:CAA26478.1; PID:g732706
A:Experimental source: cv. Boninori
A:Note: the authors translated the codon TCA for residue 86 as Leu, GAC for residue 145
R/Hirano, H.; Fukazawa, C.; Harada, K.
FEBS Lett. 181, 124-128, 1985
A:Title: The primary structures of the A4 and A5 subunits are highly homologous to that
A:Reference number: A91333
A:Accession: A91333
A:Molecule type: protein
A:Residues: 24-28, 'P', 30-81, 'L', 83-85, 'L', 87-93, 'V', 95-100, 'I', 102, 'M', 104, 'F', 106-116, '
A:Experimental source: cv. Boninori
A:Note: parts of the A4 chain, including the amino end, were sequenced
C:Comment: The source of this protein was cotyledon tissue taken from seeds at the middl
C:Comment: The glycinin molecule, the major seed storage protein of soybean, is composed
identified.
C:Comment: Acidic (A5 and A4) and basic (B3) components of this glycinin subunit are syn
sulfide bond, that is thought to be noncovalently associated with the A4 chain.
C:Superfamily: glycinin

Query Match 100.0%; Score 38; DB 1; Length 562;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
Db 543 NWGPLV 548

RESULT 4
S20946
Glycinin Gy4 precursor - soybean (cv. Forrest)
C:Species: Glycine max (soybean)
A:Variety: cv. Forrest
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
R/Xue, Z.T.; Xu, M.L.; Shen, W.; Zhuang, N.L.; Hu, W.M.; Shen, S.C.
C:Accession: S20946
Plant Mol. Biol. 18, 897-908, 1992
A:Title: Characterization of a Gy4 glycinin gene from soybean Glycine max cv. Forrest.
A:Reference number: S20946; MUID:92256811; PMID:1316192
A:Accession: S20946
A:Molecule type: DNA
A:Residues: 1-562 <XUE>
A:Cross-references: UNIPROT:Q43452; EMBL:X52863; NID:g18640; PIDN:CAA37044.1; PID:g18641
A:Experimental source: cv. Forrest
C:Genetics:
A:Gene: Gy4
A:Introns: 97/1; 184/3; 433/3
C:Superfamily: glycinin

C:Keywords: seed; storage protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-562/Product: glycinin Gy4 #status predicted <MAT>

Query Match 100.0%; Score 38; DB 2; Length 562;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
Db 543 NWGPLV 548

RESULT 5
S54802
glycinin A5A4B3 chain - soybean
C:Species: Glycine max (soybean)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S54802
R/Xue, Z.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54802
A:Accession: S54802
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-563 <XUE>
A:Cross-references: UNIPROT:Q39921; EMBL:X86970; NID:g806555; PIDN:CAA60533.1; PID:g8065
C:Superfamily: glycinin

Query Match 100.0%; Score 38; DB 2; Length 563;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
Db 544 NWGPLV 549

RESULT 6
I41169
colicin A - Escherichia coli (fragments)
C:Species: Escherichia coli
C>Date: 31-May-1996 #sequence_revision 25-Oct-1996 #text_change 09-Jul-2004
C:Accession: I53544; I41169
R/Geli, V.; Llobes, R.; Zaai, S.A.; van Spaendonk, R.M.; Rollin, C.; Benedetti, H.; La
FEBS Microbiol. Lett. 109, 335-342, 1993
A:Title: Recognition of the colicin A N-terminal epitope ICL1 in vitro and in vivo in Es
A:Reference number: I53544; MUID:93339568; PMID:7687969
A:Accession: I53544
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: UNIPROT:Q47108; EMBL:X73248; NID:g312557
R/Baty, D.; Knibbeler, M.; Verheij, H.; Fattus, F.; Shire, D.; Bernadac, A.; Lazdunski,
Proc. Natl. Acad. Sci. U.S.A. 84, 1152-1156, 1987
A:Title: Site-directed mutagenesis of the COOH-terminal region of colicin A: Effect on
A:Reference number: I41169; MUID:87147231; PMID:2434951
A:Accession: I41169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 20-223 <RE2>
A:Cross-references: GB:M15691; NID:g145562; PIDN:AAA23592.1; PID:g145563
C:Superfamily: colicin IB
C:Keywords: bacteriocin

Query Match 92.1%; Score 35; DB 2; Length 223;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
Db 148 NWGPLV 153

```

RESULT 7
colicin N - Escherichia coli plasmid pCHAP4
C:Species: Escherichia coli
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: S00867
R:Pugaley, A.P.
Mol. Microbiol. 1, 317-325, 1987
A:Title: Nucleotide sequencing of the structural gene for colicin N reveals homology bet
A:Reference number: S00867; MUID:88201670; PMID:2834623
A:Accession: S00867
A:Molecule type: DNA
A:Residues: 1-387 <PUG>
A:Cross-references: UNIPROT:P08083; EMBL:Y00533; NID:g41115; PIDN:CAA68592.1; PID:g41116
C:Genetics:
A:Gene: cna
A:Genome: plasmid
C:Keywords: bacteriocin; transmembrane protein

Query Match 92.1%; Score 35; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
Db 313 NWGPLL 318

RESULT 8
IKSCBB
colicin B - Escherichia coli plasmid ColBM-pF166
C:Species: Escherichia coli
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: A27089
R:Schrann, E.; Mende, J.; Braun, V.; Kamp, R.M.
J. Bacteriol. 169, 3350-3357, 1987
A:Title: Nucleotide sequence of the colicin B activity gene cba: consensus pentapeptide
A:Reference number: A27089; MUID:87250309; PMID:2439491
A:Accession: A27089
A:Molecule type: DNA
A:Residues: 1-511 <SCH>
A:Cross-references: UNIPROT:P05819; GB:M16816; NID:g145566; PIDN:AAA98063.1; PID:g145567
C:Comment: Colicins are plasmid-encoded proteins that kill sensitive strains of E. coli
cytoplasmic membrane, leading to dissipation of cellular energy.
C:Genetics:
A:Gene: cba
A:Genome: plasmid
C:Superfamily: colicin IB
C:Keywords: antibiotic; bacteriocin; toxin; transmembrane protein

Query Match 92.1%; Score 35; DB 1; Length 511;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
Db 439 NWGPLM 444

RESULT 9
IKESCA
colicin A - Citrobacter freundii (strain CA31) plasmid Cola
C:Species: Citrobacter freundii
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: I40784; A03504; I40777
R:Morlon, J.; Chartier, M.; Bidaud, M.; Lazdunski, C.
Mol. Gen. Genet. 211, 231-243, 1988
A:Title: The complete nucleotide sequence of the colicinogenic plasmid Cola. High extent
A:Reference number: I40778; MUID:88174422; PMID:2832701
A:Accession: I40784
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-592 <RES>
A:Cross-references: UNIPROT:P04480; GB:M37402; NID:g144661; PIDN:AAA72879.1; PID:g144662
A:Experimental source: plasmid Cola
R:Morlon, J.; Iloubes, R.; Varenne, S.; Chartier, M.; Lazdunski, C.
J. Mol. Biol. 170, 271-285, 1983
A:Title: Complete nucleotide sequence of the structural gene for colicin A, a gene tran
A:Reference number: A03504; MUID:84036205; PMID:6313941
A:Accession: A03504
A:Molecule type: DNA
A:Residues: 1-592 <MOR>
A:Cross-references: GB:X01008; GB:X00034; NID:g40459; PIDN:CAA25503.1; PID:g40460
R:Morlon, J.; Iloubes, R.; Chartier, M.; Bonicel, J.; Lazdunski, C.
EMBO J. 2, 787-789, 1983
A:Title: Nucleotide sequence of promoter, operator and amino-terminal region of caa, th
A:Reference number: I40777; MUID:84057757; PMID:6641715
A:Accession: I40777
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-53, 'X', 55-70 <RE2>
A:Cross-references: GB:M26369; NID:g144659; PIDN:AAA98057.1; PID:g144660
A:Experimental source: plasmid Cola
C:Comment: This protein acts to depolarize the bacterial inner membrane, most likely by
C:Genetics:
A:Gene: caa
A:Genome: plasmid
C:Superfamily: colicin IB
C:Keywords: antibiotic; bacteriocin; toxin; transmembrane protein

Query Match 92.1%; Score 35; DB 1; Length 592;
Best Local Similarity 83.3%; Pred. No. 84;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
Db 517 NWGPLM 522

RESULT 10
E84708
probable signal peptidase I [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 03-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84708
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Varakan, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84708
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <STO>
A:Cross-references: UNIPROT:O04348; GB:AE002093; NID:g1946373; PIDN:AAB63091.1; GSPDB:
C:Genetics:
A:Gene: At2g30440
A:Map position: 2

Query Match 89.5%; Score 34; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPL 5
Db 209 NWGPL 213

RESULT 11
P84071
hypothetical protein BH3374 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: P84071
```

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84071
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-265 <STO>
A;Cross-references: UNIPROT:Q9K717; GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BA8070
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3374

Query Match 89.5%; Score 34; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPL 5
Db 172 NWGPL 176

RESULT 12
E86203
probable signal peptidase [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86203
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86203
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <STO>
A;Cross-references: UNIPROT:Q9M922; GB:AE005172; NID:g7523697; PIDN:AAF631136.1; GSPDB:GN
C;Genetics:
A;Map position: 1

Query Match 89.5%; Score 34; DB 2; Length 367;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPL 5
Db 326 NWGPL 330

RESULT 13
PS0154
125K surface antigen M17 - *Entamoeba histolytica* (fragment)
C;Species: *Entamoeba histolytica*
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: PS0154
R;Edman, U.; Meraz, M.A.; Rausser, S.; Agabian, N.; Meza, I.
J. Exp. Med. 172, 879-888, 1990
A;Title: Characterization of an immuno-dominant variable surface antigen from pathogenic
A;Reference number: JH0284; MUID:90354789; PMID:1696956
A;Accession: PS0154
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-471 <EDM>
A;Cross-references: UNIPROT:Q05351
A;Experimental source: strain REF291

Query Match 89.5%; Score 34; DB 2; Length 471;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPL 5
Db 45 NWGPL 49

RESULT 14
T50435
conserved hypothetical protein SPCC4B3.13 [imported] - fission yeast (*Schizosaccharomyces*
C;Species: *Schizosaccharomyces pombe*
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50435
R;Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, November 1999
A;Reference number: Z25033
A;Accession: T50435
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-539 <SEE>
A;Cross-references: UNIPROT:Q9USK3; EMBL:AL132870; PIDN:CAB60687.1; GSPDB:GN00068; SPDB:
A;Experimental source: strain 972h(-); cosmid c4B3
C;Genetics:
A;Gene: SPDB:SPCC4B3.13
A;Map position: 3

Query Match 89.5%; Score 34; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPL 5
Db 318 NWGPL 322

RESULT 15
D70413
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain nuod2 [similarity] - *Aquifex aeolicus*
C;Species: *Aquifex aeolicus*
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 12-Jul-2004
C;Accession: D70413
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70413
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-586 <AQF>
A;Cross-references: UNIPROT:O67335; GB:AE000734; NID:g2983733; PIDN:AAC07298.1; PID:g298
A;Experimental source: strain VF5
C;Genetics:
A;Gene: nuod2
C;Superfamily: [NiFe]-hydrogenase-3-type complex, fused large subunit/NADH:quinone oxid
C;Keywords: NAD; oxidoreductase

Query Match 89.5%; Score 34; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPL 5
Db 202 NWGPL 206

Search completed: November 6, 2004, 19:54:13
Job time : 15.625 secs